

Benjamin J Callahan

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Population Health and Pathobiology
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Education

- 2009 **Ph.D. in Physics**
University of California, Santa Barbara
Advisor: Dr. Boris Shraiman
Dissertation: *Evolution on an interacting fitness landscape: The effects of the interplay of epistasis and recombination on genetic structure*
- 2002 **B.S. in Physics and Math**, With distinction
Iowa State University
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Research Experience

- 2017- Assistant Professor, NC State University, Population Health and Pathobiology
- 2014-2016 Research Associate (staff), Stanford University, Statistics
- 2010-2013 Postdoctoral Scholar, Stanford University, Applied Physics
- 2005 - 2009 Research Assistant, UC Santa Barbara, Physics
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Teaching Experience

- 2015 Teaching Assistant, Marine Biological Laboratory (Woods Hole)
Strategies and Techniques for Analyzing Microbial Population Structure
- 2003-2009 Teaching Assistant, UC Santa Barbara
Intro Physics, Classical Mechanics, Statistical Mechanics (graduate)

Publications

Callahan BJ, McMurdie PJ, Holmes SP (2017). Exact sequence variants should replace operational taxonomic units in marker gene data analysis. *bioRxiv* 113597.

Mayer-Blackwell K, Fincker M, Molenda O, **Callahan BJ**, Sewell H, Holmes S, Edwards E, Spormann A. 1,2-dichloroethane exposure alters the population structure, metabolism, and kinetics of a trichloroethene-dechlorinating *Dehalococcoides mccartyi* consortium (2016). *Environmental Science & Technology*, 50:12187–12196.

Callahan BJ, Sankaran K, Fukuyama JA, McMurdie PJ, Holmes SP (2016). Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. *F1000 Research* 5:1492.

Callahan BJ, McMurdie PJ, Rosen MJ, Han AW, Johnson AJ, Holmes SP (2016). DADA2: High resolution sample inference from Illumina amplicon data. *Nature Methods* 13, 581–583.

Bik EM, Costello EK, Switzer AD, **Callahan BJ**, Holmes SP, Wells RS, Carlin KP, Jensen ED, Venn-Watson S, Relman DA (2016). Marine mammals harbor novel microbiotas shaped by, yet distinct from, the sea. *Nature Communications* 7, 10516.

Callahan BJ, Proctor D, Relman DA, Fukuyama J, Holmes SP (2016). Reproducible research workflow in R for the analysis of personalized human microbiome data. *Pacific Symposium on Biocomputing* 21, 183-194.

DiGiulio DB*, **Callahan BJ***, McMurdie PJ, Costello EK, Lyell DJ, Robaczewska A, Sun CL, Goltsman DSA, Wong RJ, Shaw G, Stevenson DK, Holmes SP, Relman DA (2015). Temporal and spatial variation of the human microbiota during pregnancy. *PNAS*, 112(35), 11060-11065. (*equal contributions)

Callahan BJ, Fukami T, Fisher DS (2014). Rapid Evolution of Adaptive Niche Construction in Experimental Microbial Populations. *Evolution*, 68(11), 3307-3316.

Walker SI*, **Callahan BJ***, Arya G, Barry JD, Bhattacharya T, Grigoryev S, Pellegrini M, Rippe K, Rosenberg SM (2013). Evolutionary Dynamics and Information Hierarchies in Biological Systems. *Annals of the New York Academy of Sciences*, 1305(1): 1-17. (*equal contributions)

Rosen MJ, **Callahan BJ**, Fisher DS, Holmes SP (2012). Denoising PCR-amplified metagenome data. *BMC bioinformatics*, 13(1), 283.

Callahan BJ (2012). The length scale of selection in protein evolution. *Fly*, 6(1), 16-20.

Sellis D, **Callahan BJ**, Petrov DA, Messer PW (2011). Heterozygote advantage as a natural consequence of adaptation in diploids. *PNAS*, 108:20666-20671.

Callahan BJ, Neher RA, Bachtrog D, Andolfatto PA, Shraiman BI (2011). Correlated evolution of nearby residues in *Drosophilid* proteins. *PLoS Genetics*, 7(2): e1001315.

Callahan BJ, Thattai M, Shraiman BI (2009). Emergent gene order in a model of modular polyketide synthases. *PNAS*, 106:19410-19415.

Cheung MS, Finke JM, **Callahan BJ**, Onuchic JN (2003). Exploring the interplay between topology and secondary structural formation in the protein folding problem. *Journal of Physical Chemistry B*, 107:1193-11200.

Honors and Awards

2015	Microbiome Seed Grant, Samarth Foundation
2015	Pacific Symposium on Biocomputing Travel Award
2003 - 2005	Broida Fellowship for Graduate Studies in Physics
before 2002	Phi Beta Kappa, Tau Beta Pi, National Merit Scholarship

Invited Talks

2017	Joint Statistical Meetings
2017	University of Idaho Seminar for the Center for Modeling Complex Interactions (CMCI) and the Institute for Bioinformatics and Evolutionary Studies (IBEST)
2017	UNC Biostatistics Seminar
2016	Stanford Bioinformatics for the Microbiome Symposium
2016	Simons Foundation Challenges in Microbiome Data Analysis
2015	Harvard University Workshop on Metagenomics
2015	Johnson & Johnson Microbiome Workshop
2014	American Society of Naturalists Meeting (Best postdoc talk, 2nd/3rd)
2012	REvolution - Transcending the Past Symposium
2011	Vienna Institute of Science and Technology
2010	Bay Area Population Genomics Meeting, Berkeley
2009	Princeton University

Professional Activities

Reviewer: Proceedings of the Royal Society B, Theoretical Population Biology, PLoS One, Genetics, Frontiers in Genetics, PeerJ, Bioinformatics, Microbiome, mSystems

Mentoring: Mike McLaren (postdoc), Michael Rosen (PhD), Joel Thompson (MS), Katie Lund (undergraduate)